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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/687,060

DATE: 08/27/2004

TIME: 11:52:32

Input Set : N:\Crf3\RULE60\10687060.raw
 Output Set: N:\CRF4\08272004\J687060.raw

1 <110> APPLICANT: Bruck, Claudine
 2 Godart, Stephane Andre Georges
 3 Marc-Hand, Martine
 4 <120> TITLE OF INVENTION: Fusion Proteins Comprising HIV-1 TAT
 5 and/or Nef Proteins
 6 <130> FILE REFERENCE: B45110
 7 <140> CURRENT APPLICATION NUMBER: US/10/687,060
 8 <141> CURRENT FILING DATE: 2003-10-16
 9 <150> PRIOR APPLICATION NUMBER: US/09/509,239
 10 <151> PRIOR FILING DATE: 2000-03-23
 11 <150> PRIOR APPLICATION NUMBER: PCT/EP98/06040
 12 <151> PRIOR FILING DATE: 1998-09-17
 13 <150> PRIOR APPLICATION NUMBER: GB 9720585.0
 14 <151> PRIOR FILING DATE: 1997-09-26
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 16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 23
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 21 <213> ORGANISM: Pichia pastoris
 22 <400> SEQUENCE: 1
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 26 <211> LENGTH: 23
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Pichia pastoris
 29 <400> SEQUENCE: 2
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 33 <211> LENGTH: 24
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Pichia pastoris
 36 <400> SEQUENCE: 3
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 39 <210> SEQ ID NO: 4
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 42 <213> ORGANISM: Pichia pastoris
 43 <400> SEQUENCE: 4
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 46 <210> SEQ ID NO: 5
 47 <211> LENGTH: 23
 48 <212> TYPE: DNA

ENTERED
EN

23

23

24

24

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 56 <213> ORGANISM: *Pichia pastoris*
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 59 agccattcat caaatatggc gaatacccaa atgaaatca gacaaatcat tattgctcac 120
 60 cgtggtgcta gcggtttattt accagagcat acgttagaat ctaaaggact tgctttgca 180
 61 caacaggctg attatttaga gcaagattta gcaatgacta aggatggctg ttttagtggtt 240
 62 attcacgatc actttttaga tggcttgact gatgttgcga aaaaattccc acatcgcat 300
 63 cgtaaagatg gccgttacta tgtcatcgac ttaccttaa aagaaattca aagtttagaa 360
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 74 Ala Gly Cys Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys
 75 20 25 30
 76 Ser Asp Lys Ile Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro
 77 35 40 45
 78 Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp
 79 50 55 60
 80 Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
 81 65 70 75 80
 82 Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
 83 85 90 95
 84 Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
 85 100 105 110
 86 Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
 87 115 120 125
 88 Ala Thr Cys Asp Gln Ser Ser Thr Ser Gly His His His His His His
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 97 agacgagctg agccagcagc agatgggtg ggagcagcat ctcgagacat ggaaaaacat 120
 98 ggagcaatca caagtagcaa tacagcagct accaatgctg cttgtgcctg gctagaagca 180
 99 caagaggagg aggaggtgg tttccagtc acacctcagg tacctttaag accaatgact 240
 100 tacaaggcag ctgttagatct tagccactt taaaagaaa agggggact ggaaggcata 300

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101	attcactccc aacgaagaca agatatcctt gatctgtgga tctaccacac acaaggctac	360
102	ttccctgatt ggcagaacta cacaccagg ccaggggtca gatatccact gacctttgga	420
103	tgggtctaca agcttagtacc agttgagcca gataaggtag aagaggccaa taaaggagag	480
104	aacaccagct tggcaccc tggagccctg catggaatgg atgaccctga gagagaagtg	540
105	ttagagtgga ggtttgacag ccgcctagca tttcatcag tgcccgaga gctgcatccg	600
106	gagacttca agaactgcac tagtggccac catcaccatc accattaa	648
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115	Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala	
116	20 25 30	
117	Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr	
118	35 40 45	
119	Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu	
120	50 55 60	
121	Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr	
122	65 70 75 80	
123	Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly	
124	85 90 95	
125	Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu	
126	100 105 110	
127	Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr	
128	115 120 125	
129	Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys	
130	130 135 140	
131	Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu	
132	145 150 155 160	
133	Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro	
134	165 170 175	
135	Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His	
136	180 185 190	
137	His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser	
138	195 200 205	
139	Gly His His His His His	
140	210 215	
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145 <213>	ORGANISM: Pichia pastoris	
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148	gcttgtacca attgctattg taaaaagtgt tgctttcatt gccaagtttg tttcataaca	120
149	aaagccttag gcatctccta tggcaggaag aagcggagac agcgcacgaag acctcctcaa	180
150	ggcagtca gtcataacta aagcaaccca cctcccaatc ccgagggac	240
151	ccgacaggcc cgaaggaaac tagtggccac catcaccatc accattaa	288

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Output Set: N:\CRF4\08272004\J687060.raw

153 <210> SEQ ID NO: 11
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 156 <213> ORGANISM: *Pichia pastoris*
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 160 Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
 161 20 25 30
 162 His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly
 163 35 40 45
 164 Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
 165 50 55 60
 166 His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Arg Gly Asp
 167 65 70 75 80
 168 Pro Thr Gly Pro Lys Glu Thr Ser Gly His His His His His His His
 169 85 90 95

171 <210> SEQ ID NO: 12
 172 <211> LENGTH: 909
 173 <212> TYPE: DNA
 174 <213> ORGANISM: *Pichia pastoris*
 175 <400> SEQUENCE: 12
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 177 agacgagctg agccagcagc agatgggtg ggagcagcat ctcgagacat ggaaaaacat 120
 178 ggagcaatca caagtagcaa tacagcagct accaatgctg cttgtgcctg gctagaagca 180
 179 caagaggagg aggaggtggg tttccagtc acacccagg tacctttaag accaatgact 240
 180 tacaaggcag ctgttagatct tagccacttt taaaaagaaa agggggact ggaagggcta 300
 181 attcactccc aacgaagaca agatatcctt gatctgtgga tctaccacac acaaggctac 360
 182 ttccctgatt ggcagaacta cacaccagg ccaggggtca gatatccact gacctttgga 420
 183 tggtgctaca agcttagtacc agttgagcca gataaggtag aagaggccaa taaaggagag 480
 184 aacaccagct tggcaccc tggcgcctg catggaatgg atgaccctga gagagaagtg 540
 185 ttagagtgga ggtttgacag ccgcctagca tttcatcagc tggcccgaga gctgcatccg 600
 186 gagtaattca agaactgcac tagtgagcca gtatgccta gactagagcc ctggaaagcat 660
 187 ccaggaagtc agcctaaaac tgcttgatc aattgttatt gtaaaaaagtg ttgcttcat 720
 188 tgccaagtt gttcataac aaaagccta ggcatctcct atggcaggaa gaagcggaga 780
 189 cagcgcacgaa gacctcctca aggcaatcag actcatcaag tttctctatc aaagcaaccc 840
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 194 <211> LENGTH: 302
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 196 <213> ORGANISM: *Pichia pastoris*
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 200 Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala
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 202 Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr
 203 35 40 45

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204 Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu
 205 50 55 60
 206 Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
 207 65 70 75 80
 208 Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
 209 85 90 95
 210 Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
 211 100 105 110
 212 Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
 213 115 120 125
 214 Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
 215 130 135 140
 216 Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu
 217 145 150 155 160
 218 Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro
 219 165 170 175
 220 Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
 221 180 185 190
 222 His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser
 223 195 200 205
 224 Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln
 225 210 215 220
 226 Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
 227 225 230 235 240
 228 Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg
 229 245 250 255
 230 Lys Lys Arg Arg Gln Arg Arg Pro Pro Gln Gly Ser Gln Thr His
 231 260 265 270
 232 Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Arg Gly Asp Pro
 233 275 280 285
 234 Thr Gly Pro Lys Glu Thr Ser Gly His His His His His His
 235 290 295 300
 237 <210> SEQ ID NO: 14
 238 <211> LENGTH: 1029
 239 <212> TYPE: DNA
 240 <213> ORGANISM: Pichia pastoris
 241 <400> SEQUENCE: 14
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 244 cgtggtgcta gcggttattt accagagcat acgttagaat ctaaagcaact tgctttgca 180
 245 caacaggctg attatttaga gcaagattta gcaatgacta aggatggctcg tttagtggtt 240
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 247 cgtaaagatg gccgttacta tgtcatcgac tttaccttaa aagaaattca aagtttagaa 360
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 252 gtacctttaa gaccaatgac ttacaaggca gctgttagatc tttagccactt tttaaaagaa 660
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RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

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Seq#:2; Line(s) 30
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Seq#:4; Line(s) 44
Seq#:5; Line(s) 51
Seq#:6; Line(s) 58,59,60,61,62,63,64,65
Seq#:8; Line(s) 96,97,98,99,100,101,102,103,104,105,106
Seq#:10; Line(s) 147,148,149,150,151
Seq#:12; Line(s) 176,177,178,179,180,181,182,183,184,185,186,187,188,189
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Seq#:14; Line(s) 256,257,258,259
Seq#:16; Line(s) 313,314,315,316,317,318,319,320,321,322,323,324,325,326
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Seq#:20; Line(s) 484,485,486,487,488,489,490
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Seq#:24; Line(s) 584,585,586,587,588,589,590,591,592,593,594,595,596,597
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Seq#:26; Line(s) 650

VERIFICATION SUMMARY

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